

 ${f Fig}$ 1

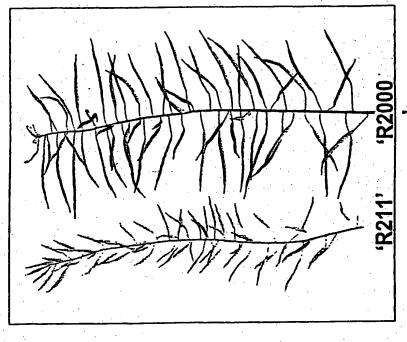


Fig. 1: Seed set on 'R211' and 'R2000'

| Genotype | Selfings | Test Crosses |
|----------|---------------------|--------------------|
| Drakkar | 29.3 | |
| Pactol | 23.1 | |
| R211 | 11.2 | 25.5 |
| R2000 | 26. 5 (24.0 – 31.1) | 27.0 (24.0 – 28.7) |

Fig 3

| - | d | ۲ |
|---|---|---|
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|----------|--|---|---|--|--|---|--|--|
| į | 130 -16CC16TC -16CC16TC -CGCC16TC | SCCTSTC SCCTCTC SCCTCTC SCCTCTC SCCTCTC | 260 1 1 100 TTT 10 | RABITTG RABITTG RABITTG RABITTG RABITTG RABITTG RABITTG RABITTG RABITTG | 86 18 88 | CATGATT CATGATT CATGATT CATGATT CATGATT | | |
| C | | 164C161C161C161C161C161C161C161C161C161C | 250 TTGTGRITT | | 380 T6666811 T6666811 | 1666681 1666681 1666681 1666681 1666681 | • | |
| 110 | 76116 76116 76116 76116 76116 | 716776- 17677676 17677676 17677676 17677676 | 240 GTATGRAT GTATG | THICARI TRICARI TRICARI TRICARI TRICARI TRICARI | 370 CCATGTTC1 CCATGTTC1 CCATGTTC1 | CRIGITCI CRIGITCI CRIGITCI CRIGITCI CRIGITCI CRIGITCI CRIGITCI | - - | TCARR |
| | TCATTIGATIGTIG | CATTGA CATTGA CATTGA CATTGA | CRECACTANTETTGCGGTATG | 11CT16C6C 11CT16C6C 11CTT6C6C 11CTT6C6C 11CTT6C6CC 11CTT6C6CCCCCCCCCC | CTABICTO | CTRBTCTC CTRBTCTC CTRBTCTC CTRBTCTC CTRBTCTC | } | GCAAGGCE |
| 100 | TTGTATT | TTTBTT TGTRTT TGTRTT TGTRTT TGTRTT | 230 SCRCTRIN SCRCTRIN | CACTAR CACTAR CACTAR CACTAR CACTAR | 360 FACARTG FACARTG | INCRATE INCRATE INCRATE INCRATE | 280 ABOCHB | IARCAR IRACAR IRRCAR |
| 90 | CRITGAGGARITGGATTACARCIGCTCTTGGGTTAGTATCTCTCTTTGCTTAGCGTCCARATTTCATGATTGTTGTTTGATTGATTGATTGATTGATTGA | CRITGAGGARITGGATTACHACTGCTCTTGGCTTAGGATCANTCTCTTTGCTTGCTCTGARATTTGATGATTGATGATGATGATGATGATGATGATGATGA | 150 170 180 190 200 210 220 230 240 250 260 100 100 100 100 100 100 100 100 100 1 | RIGARCAGCAGITTARCAIGGITARCITARCAGGGCTCCGGCTGTTGCARARCACHIGGITGCTGTCAGCACTARICTIGCGGTATGARITIGTGATTARATTTG RIGARCAGCAGICATTARCAIGGTTARCTAGGGCTCCGGCTGTTGCARARCACTAGTTGCTGTCGAGCARATCTGCGGTATGARITIGTGATTARATTTG RIGARCAGCAGTCATTARCAIGGTTARCTARCAGGGCTCCGGCTGTTGCARARCATAGTGTTGCTGTGTGTGTATATTTGCGGTATGARTTTGTGATTARATTTG RIGARCAGCAGTCATTARCATARCAGGGTTARCTARCAGGGCTCCGGCTGTTGCARARCATAGTTGCTGTGCTARATCTTGCGGTATGARTTTGTGATTARATTTG RIGARCAGCAGTATTARCATARCATAGGGTTARCTTARCAGGGCTCCGGCTGTTGCARARCATAGTTGCTGTGCTARATCTTGCGGTATGARTTTGTGATTARATTTG RIGARCAGCAGTATTARCATGGGGTTARCTTARCAGGGCTCCGGCTGTTGCARARCATATGTTGTTGTTGTTGTTGTGATTTGTGATTTARATTTG RIGARCAGCAGTATARCATAGGGGTTARCTTARCAGGGCTCCGGCTGTTGCARARCATATGGTTGTTGTTGTATTTGTGATTTARATTTG RIGARCAGCAGCAGCACACACACACACACACACACACACACA | 7 290 300 310 320 330 340 350 350 390 390 350 350 360 370 380 390 700 100 100 100 100 100 100 100 100 10 | TCATTGITCGITCTGIACRAIRANCCORRIGIAIRAICTITITACRARCTGRATITTCIACCGGGTCTGATGTACARIGCTAGITCCTGGGGGTTCTTGGGGATCATGATT TCATTGITCGITTTGGTACRAIRANCCGARGTATRACCTITTTACRARCTGARGTCTCTCGGGGTCGTGTTGTTTGGTAGTT TCATTGITCGITTTCGTACTATRANCCGARGTATRACCTITTTACARACTGARATGTCTACCGGGTCTGATGTACARATGCTAGTCTTCGGGGATCATGATT TCATTGTTCGTTTTCGTACARATARACCGARTGATARACCTTTTTACARACTGARATGTTACCGGGTCGTGTTGCTAGTCTCCATGTTCTTGGGGATCATGATT TCATTGTTCGTTTTCGTRCARTARACCGARTGATARACTTTTTACARACTGARATGTTACCGGGTCGTTGTTACTTGTTTTTGGGGATCATGATTACARACTGARATGTTACCAGGGTCATGATACTAGTTTTTGGGGATCATGATACTAGTTTTTGGGGATCATGATACAAAAAAAA | ASO 480 49 RICHGTRICHGRARHRUTRITTTRRRRCTCTGGRTGTTTTRATTTRCHGTTRGTGGRGGRGTTCGGCRTTGRTCC RICHGTRICHGRARGTRTTTRAHRUCTCTGGRTGTTTTRRTTTRCHGTTGGRGGRGGTTCGGCRTTGRTCCCARCAR | ACRGTACRGARGARRGTGTTCARRACICTGGATGTTTTARTTACRGTTRGTGGAGARGTTCGGCATTGATCC ACRGTACRGARGARATGTTTARRACICTGGATGTTTTGATTTACAGTTAGTGGAGARGTTGGAGATGTTGATCCGAACAR ACRGTACRGARGARARATGTTTARRACICTGGATGTTTTTGATTTACAGTTRG-GGAGAGATTGGTTGATCCGAACARTGCAAGAGATCAAR ACRGTACAGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| 80 | CGTCCBBB CGTCCBBB CGTCCBBB | CGTCCRR CGTCCRR CGTCCRR CGTCCRR CGTCCRR | CACATGGT | CACATGGT CACATGGT CATATGGT CATATGGT CATATGGT 00.02 | 340 TCTRCCGG TCTRCCGG | TCTACCGG TCTACCGG TCTACCGG TCTACCGG | ACHO 480 480 480 480 480 480 480 480 480 480 | ACAGTACAGARGARAGIGITCARARCICICIGARIGITITARITIACAGITRGIGGAGARGITCGCCATICATCCACAGARGATCGCCATICATCCACAGARGATCCATTAGATCCATTAGATCCATTAGATCCATTAGATCCATTAGATCCATTAGATCAGATAGAT |
| . , | TGCTTRG TGCTTRG TGCTTRG | TOCTTRO TOCTTRO TOCTTRO Lectte | TGCRABA | 16CABA 16CABA 16CABA 16CABA 16CABA 16CABA | TEARTTT TT TGARTTT | 168816 168816 168816 168816 168816 168816 | 616GAGA 616GAGA 616GAGA | 6166868 0166868 0-66868 6166868 |
| 70 | | CICICIT | 200 RGGCTGT | CGGCTGT CGGCTGT CGGCTGT CGGCTGT CGGCTGT CGGCTGT CGGCTGT CGGCTGT CGGCTGT | 330 TRCARRC TRCARRC | TACRARC TACRARC TACRARC TACRARC CACABAC | AGO ACAGITA ACAGITA ACAGITA | ACRETTA ACRETTA ACRETTA ACRETTA |
| 09 | TRICIAL | TATCTAL TRICTAL TRICTAL TRICTAL | 190 :RGGGCTC | #666CTC #666CTC #666CTC #666CTC | 320 RICTITI | RCCTTT RCCTTTT RCCTTTT BCCTTTT B. otter | 450 TTBRITT TTBRITT | TTRBTTT TTGBTTT TTGBTTT TTGBTTT |
| 20 | GGGTTRC GGGTTRC GGGTTRC | 666178 666178 666178 666178 | HCTTARC | ECTTER BCTTER BCTTER BCTTER BCTTER BCCTER | O. BTBTRIFF BTGTRIFF BTGTRIFF | ATCTATE ATCTATE ATCTATE ATCTATE OCCCO | GGATGTT GGATGTT GGATGTT | GGRIGIT GGRIGIT GGRIGIT GGRIGIT |
| | 16CTCTT 16CTCTT 16CTCTT | 160101 160101 160101 160101 | 180 (9166118) (9166118) | GTGGTTF GTGGTTF GTGGTTF GTGGTTF GTGGTTF GTGGTTF GTGGTTF | 310 BARCCGAR RARCCGAR | HRACCGA HRACCGA HRACCGA HRACCGA HRACCGA | AND | RESCICT RESCICT RESCICT RESCICT |
| 8 | ATTACARC BTTACARC BTTACARC | HTTACAR HTTACAR HTTACAR ATTACAR St. acas | 170 ITTRRCRI | TTARCA TTARCA TTARCA TTARCA TTARCA TTARCA Starca | 300 GTACARI GTACARI | GINCRN GINCRN GINCRN GINCRN GINCRN STRCRN | METATTER METATTER METATTER | 161617CA 181617TA 181617TA |
| 30 | GARTTGG GARTTGG GARTTGG | GARTTGG GARTTGG GARTTGG GARTTGG | 160 GCRGTCR GCRGTCR | GCRGTCA GCRGTCA GCRGTCA GCRGTCA GCRGTCA GCRGTCA | TCGTTTT | TCGTTTT TCGTTTT TCGTTTT TCGTTTT TCGTTTT TCGTTTTT | NGARGARI NGARGARI NGARGARI | RGARGARA RGARGARA RGARGARA RGARGARA |
| | CATTGAG CATTGAG TGAG TGAG | CATTGAG CATTGAG TTGAG TTGAG | ятеляся ятеляся | ATGRACA ATGRACA ATGRACA ATGRACA ATGRACA ATGRACA | TCATTGT TCATTGT | TCATTGT TCATTGT TCATTGT TCATTGT TCATTGT LOALLEL | ACRETAC ACRETAC | ACAGTACAGAAG ACAGTACAGAAG ACAGTACAGAAG ACAGTACAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG |
| . ଅ | | EE . | | | | CTTT-CTTT-CTTT-CTTT-CTTT-CTTT-CTTT-CTT | | |
| 10 | ТЯПЯСЯЯТССТТАМСВСЯБ | ТАВСАЛ ОСТТАНСБСАБ. | 131 140 15 1 16 16 16 16 15 15 15 15 15 15 15 15 15 15 15 15 15 | GCC | 261 270 28 | TTTGTTGTGACTCTTT-CT TTGTTGTGACTCTTTCT TTGTTGTGACTCTTTTCT TTGTTGTGACTCTTTTCT TTGTTGTGACTCTTTTC ELEELEGESACCTLL.ct | TATTICTACATGIATICAL TATTICTACATGIATICAL | TATTICIACOTGIATICAG INTITICIACATGIATICAG INTITICIACATGIATICAG INTITICIACAGIATICAG EALLECAGALALAAG |
| <u> </u> | ТАВАСЯ | TARCA | 600 TIG | 6CCTTG 6CCTTG 6CCTTG 6CCTTG 6CCTTG 6CCTTG | 261 1110111 1110111 | 111G11 111G11 111G11 111G11 111G11 111G11 | | INTERIOR DE L'ACTE CONTRA L'AC |
| | prinerPGIINTU rinerentiPGII rinerentiPGII SGFICHOU STATEPPGIU SGGreebajo | M:AF258278 SGPGInav EMRF258276 SGdraariba Consensus | olEH:RF258277 PrinerPGIINTU riner antiPGIL SGPGICHOU | ETHY 2082/5 prinerPGIU SG4rabbajo M: RF258278 SGPGInav EMRF258276 SGGraeriba Consensus | olek:RF258277 prinerPGIINTU rinerant.IPGIL SGPGIChou erneKRF258275 prinerPG27 | SGdraabajo N:RF250278 SGPGINAV ENRF250276 SGdraariba Consensus | olen:AF258277 prinerPGIINTU rinerant.PGIL SGPGIChou larnEMR258278 | SGdraabajo M:AFE58278 SGPGInav EMAFE58276 SGdraariba Consensus |
| | PGIBolEH; RF258277 Prinstrain PGINIU Prinstrain PGIChou PGI-10arrHF258275 SGdroebajo | PulbrapaEN; NF258278 Supulnav Supulnav Supulnav Supulnav Supulnav Consensus | PGIBOLEH; RF258277 prinerent PGIL prinerent PGIL SGPGILHOU | FULTUBERNIESDEZDEZDEZDEZDEZDEZDEZDEZDEZDEZDEZDEZDEZD | POIBOJEH; RF258277 Primerant POIL SCPGICHOU POI-10ernEMF258275 | SGdraabajo PGIBrapaEM: AF280278 SGGIAAV SGGT-20276 SGdraariba Consensus | POIBOIEH: RESSB277 Priner POIINTU Priner antipoir SGPGITCHOU POI-JOANNESB275 PRI-TORNESB275 | SGdraabajo PGIBrapaEM; RF258278 SGFGTNBV PGI-2DarnEMRF258276 SGdraariba Consensus |
| | PG1 | PGIBr | PGI | PGIBr | PGI PGI-1 | PGIBr PGI-2 | PGI | PGIBr PGI-2 |
| | | • • • | | | | | | |

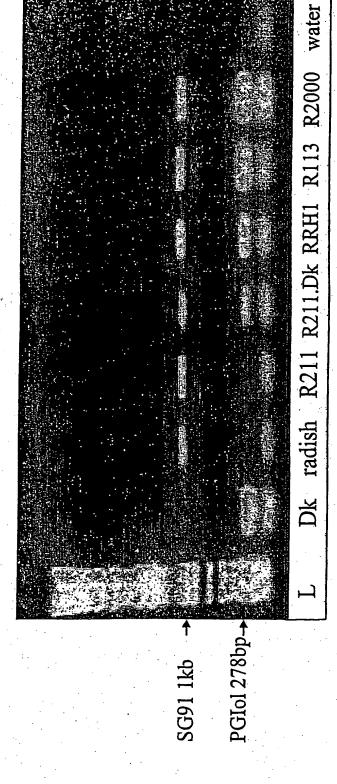
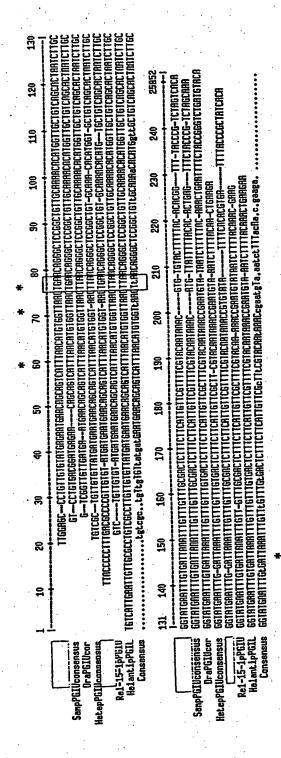
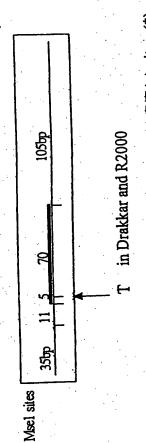


Fig.





Msel restriction enzyme cut DNA sequences at the T/TAA sites (*)

Fig 6

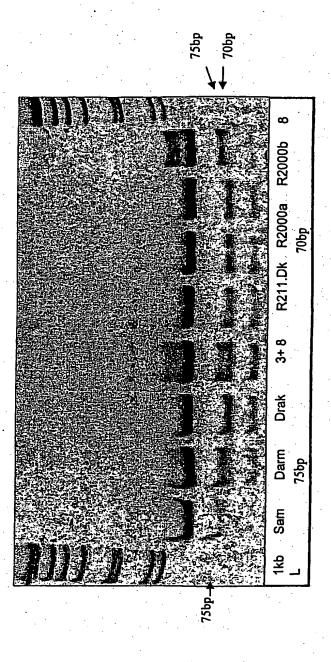


Fig 7

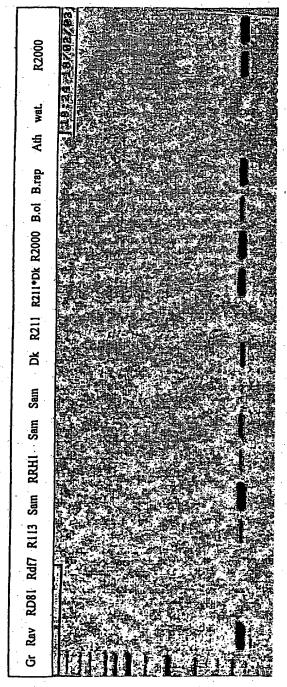


Fig 8

950bp

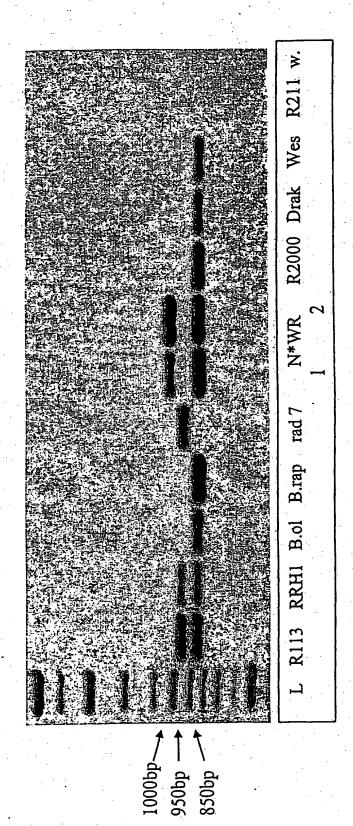


Fig 9

| ٠ | | | | | | | | | | • | | : | | | | | | |
|----------|----------------|--------------|------|-----|----|------------------|----------------|------------|----------------|--------|-------------|--------|--|--------------------------|---|---|---------------------|---|
| 7 | 14 W | | | | | 9 7 | | 290 | | | C | • | 009 | 009 | 009 | 009 | | |
| 1 | | | | | | ر | 7 | | 0 | · , | 800 | 0 | 0 | · 02 | 870 | 870 | | |
| 1 4 | | | | | | ح. | | | 870 | | | 870 | 870 | œ | ò∞ | ò | | |
| 7 | | | | | | | | | | 950 | | 950 | _ | 950 | 950 | 950 | | |
| 14 | | | | | | | | | 1 | | | - 55 | | <u> </u> | | 5 | | |
| 13 | | | | | | | | | | | | | homozygous restored rapeseed: 7 Samourai RRH1, 12 R211 | | | ine R1.15 | | |
| | | | | | | | | | | | | | KH | • . | | 9 | · . | |
| 10 11 12 | | | | | | | | | B.rapa species | | : | Pactol | amourai R | | heterozygous restored rapeseed: R211.Dk | homozygous restored R2000; 6 lineE38, 8,18,19 line R1 | | |
| | | | | 11: | I. | | | | | | | ai; 3 | : 7 S | | 2 | line | | |
| 6 | | | | | | | | | | | | nou | seed | ٠. | seed | 9 | | |
| ∞ | | | | | | | • | · | ٠ | | VS) | Sar | ape | 41 | ape | 200 | 06p | |
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| 4 | | | +150 | 7 | | (bp) | spec | RD81 | spe | icea | sdo | iner | ygo | olete | sygo | Vgo | 울 | |
| m | | | | | | nds | radish | radish | rapa | olera | abid | inta | moz | incomplete restored SRfi | teroz | moz | ladder | |
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| | | -11 | | | | Bollon PCR bands | | ٠. | | | | | | | | | | |
| | P. A. C. S. C. | | | 4 | | Jon | | | . • | | | | ~ ' | | | | 3 | |
| | • | | - | | , | Bol | 4,5 | 17 | 14 | 13 | 9 | 2,3 | 7,12 | | <u>က</u> ထ | 316 | L, L1 | |
| | | | | | | | | | | | | | | | | | | • |

It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the herterozygous R211*Dk) The CP418 band (about 650bp) specific to the B.oleracea genome. It is absent from the restored rapeseed (RRH, R113 and R211) It is present in the homozygous R2000,

Fig~11

| Political 250 Political Political | | 3 | | | | | | | | | | | | | | |
|---|-------------|--------------|--------------|------------|---------|---|---|---|---|---|---|----|---|---|---|----------------|
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| ### ### ### ### ### ### ### ### #### #### | B. ole | 950 | | | | • | • | | | + | + | | + | | | |
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| equenbe | radis | 630 | | _ | + | | | + | + | + | + | l | | | | |
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| + + + + + + + + + + + + | CP418L | | - 1 | | | | | | | | | | | | | . - |
| (approximative size band) Brassica band is characlerised by its DNA sequence | B. ole | 670 | + | | •. | + | • | • | | + | + | • | + | + | | |
| Brassica band is characlerised by its DNA sequence | (approxma | live size be |) (pue | | | _ | | | | | | | | | |] - |
| | Brassica b | and is cha | raclerised b | y its DNAs | edneuce | | | | | | | | | | | |

Figure 13 (a)

| | 51 81 PGIol U> 100 |
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| consePGIinTUNTDrakka | |
| consenswesrPGI | ********* |
| consePGIintUNTR113 | |
| consePGIintUNTBrapaA | |
| ConsePGIintUNTRRH1 | TO THE COMMENT OF THE COMMENT |
| PGIBO-EM: AF258277 | TTGCTTAGCG TCCAAATTTC ATGATTGTAT TCATTTGATT GTTGTGAC TTGCTTAGCG TCCAAATTTC ATGATTGTAT TCATTTGATT GTTGTGTGAC |
| PGIBra-EM:AF258278 consePGIintUNTBolera | TTGCTTAGCG TCCAAATTTC ATGATTGTAT TCATTTGATT GTTGTGTGAG |
| consePGIIntUNTR2000 | TTG. TCATT.GATTGT.TGCG |
| Consensus | 1 |
| | |
| | 101 |
| consePGIinTUNTDrakka | GTCG TTTGTTGGTG AGT. GAACAG CAGTCATTTA |
| consensWesrPGI | |
| consePGIintUNTR113 | |
| consePGIintUNTBrapaA | |
| ConsePGIintUNTRRH1 PGIBo-EM:AF258277 | CG TGTTGAGAAG CAG.CATTTA |
| PGIBO-EM:AF258278 | TATCGCCTC. TCGCCTTGTTG TGTTATGATG AAT.GAACAG CAGTCATTTA |
| consePGIintUNTBolera | ********* |
| consePGIintUNTR2000 | CCTG TCGCCTTGTTG TGTTATGATG AAT.GAACA. CAGTCATTTA |
| Consensus | gt.ggt.gaa.ag cagtcattta |
| | |
| | 151 Msel restriction site 200 |
| consePGIinTUNTDrakka | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG |
| consensWesrPGI | ACATG.TGGT TAACTHAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG ACATG.TGGT .AACTGAACA GGGCTCCGGC TGTTGCCC CTAAGGGTTG |
| consePGIintUNTR113 | ACATGITGGT .AACTGAACA GGGCTCCGGC TGTTGCCC CTAAGGGTTG ACATGGTGGT TAACTGAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG |
| consePGIintUNTBrapaA ConsePGIintUNTRRH1 | ACATGGGTACTGAACA GGGC.CCGGC TGTTGCAAACAGTG |
| PGIBO-EM: AF258277 | ACATG.TGGT TAACTTAACA GGGCTCAGGC TGTTGCAAAA CACATGGTTG |
| PGIBra-EM:AF258278 | ACATG. TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CATATGGTTG |
| consePGIintUNTBolera | |
| | |
| consePGIintUNTR2000 | ACATG. TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG |
| | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg |
| consePGIintUNTR2000 | ACATG. TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG |
| consePGIintUNTR2000 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| CONSEPGIINTUNTR2000 CONSENSUS CONSEPGIINTUNTDrakka | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| CONSEPGIINTUNTR2000 CONSENSUS CONSEPGIINTUNTDrakka CONSENSWESTPGI CONSEPGIINTUNTR113 CONSEPGIINTUNTBIAPAA | ACATG.TGGT TAACTTAACA GGGCTCCGCC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBO-EM:AF258277 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTBolera consePGIintUNTR2000 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTDrakka consensWesrPGI consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera consePGIintUNTR2000 Consensus consePGIintUNTDrakka | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| ConsePGIintUNTDrakka ConsensWesrPGI ConsePGIintUNTDrakka ConsePGIintUNTR113 ConsePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM: AF258277 PGIBra-EM: AF258278 ConsePGIintUNTBolera ConsePGIintUNTR2000 Consensus ConsePGIintUNTDrakka ConsePGIinTUNTDrakka | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTDrakka consensWesrPGI consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera consePGIintUNTBolera consePGIintUNTR2000 Consensus consePGIintUNTDrakka consePGIintUNTDrakka consePGIintUNTR113 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| ConsePGIintUNTDrakka ConsensWesrPGI ConsePGIintUNTDrakka ConsePGIintUNTR113 ConsePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM: AF258277 PGIBra-EM: AF258278 ConsePGIintUNTBolera ConsePGIintUNTR2000 Consensus ConsePGIintUNTDrakka ConsePGIinTUNTDrakka | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aca gggctccggc tgttgcaaaa cacatggttg 2 0 0 250 201 PGI int U> 250 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CTGTCAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CTGTCAGCAC TAATCTTGC TTCGTTTCG TACAATAAAC CGAATGTATA TGGGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CACATGTATA TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC .AATGTATA |
| ConsePGIintUNTDrakka ConsensWesrPGI ConsePGIintUNTDrakka ConsePGIintUNTR113 ConsePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM:AF258277 PGIBra-EM:AF258278 ConsePGIintUNTBolera ConsePGIintUNTR2000 Consensus ConsePGIintUNTDrakka ConsePGIintUNTDrakka ConsePGIintUNTR113 ConsePGIintUNTR113 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| consePGIintUNTR2000 Consensus consePGIinTUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 consePGIintUNTR2000 Consensus consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBo-EM:AF258277 PGIBra-EM:AF258278 | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg 2 |
| consePGIintUNTDrakka consensus consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTR2000 Consensus consePGIintUNTDrakka consePGIintUNTDrakka consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact_aaca gggctccggc tgttgcaaaa cacatggttg 2 201 PGI int U> CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CAGCACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CAATGATAA CAATGATATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAAA CAATGATAA |
| ConsePGIintUNTDrakka ConsenswsrPGI ConsePGIintUNTDrakka ConsePGIintUNTR113 ConsePGIintUNTBrapaA ConsePGIintUNTRRH1 PGIBO-EM:AF258277 PGIBra-EM:AF258278 ConsePGIintUNTBolera ConsePGIintUNTDrakka ConsePGIintUNTDrakka ConsePGIIntUNTDrakka ConsePGIIntUNTR113 ConsePGIIntUNTRH1 PGIBO-EM:AF258277 PGIBra-EM:AF258277 PGIBra-EM:AF258278 ConsePGIIntUNTBolera ConsePGIIntUNTBolera ConsePGIIntUNTBolera ConsePGIIntUNTBolera | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact.aca gggctccggc tgttgcaaaa cacatggttg 2 201 PGI int U> CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CTGTTTGTT CTGTTTCGT TACAATAAAC CGAATGTATA TGTGGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAACAATGTATA TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAACAATGTATA TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAACAATGTATA TGTGGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAACGAATGTATA TGTGGACTCTT T.CTTCATTG T |
| consePGIintUNTDrakka consensus consePGIintUNTDrakka consensWesrPGI consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTR2000 Consensus consePGIintUNTDrakka consePGIintUNTDrakka consePGIintUNTR113 consePGIintUNTBrapaA ConsePGIintUNTBrapaA ConsePGIintUNTRH1 PGIBo-EM: AF258277 PGIBra-EM: AF258278 consePGIintUNTBolera | ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG acatg.tggt taact_aaca gggctccggc tgttgcaaaa cacatggttg 2 201 PGI int U> CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT CAGCACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CAATGATAA CAATGATATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAA CAATGATAAA CAATGATAA |

Figure 13 (b)

| | 301 | < PGIol antL 341 350 |
|----------------------|--------------------|--|
| consePGIinTUNTDrakka | ATCTTTTTAC AAACTGA | |
| consensWesrPGI | ATCTTTTTAC AAACTGA | A TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| consePGIintUNTR113 | ATCTTTTTAC AAACTGA | A IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| consePGIintUNTBrapaA | ATCTTTTTAC AAACTGA | A TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| ConsePGIintUNTRRH1 | ATCTTTTTAC AAACTGA | A IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| PGIBO-EM: AF258277 | ATCTTTTTAC AAACTGA | A IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| PGIBra-EM:AF258278 | ACCTTTTTAC AAACTGA | A AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| consePGIintUNTBolera | ATCTTTTTAC AAACTGA | A TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC |
| consePGIintUNTR2000 | ATCTTTT.AC AAACTGA | |
| Consensus | atcttttac aaactgaa | tt ttctaccggg tctgatgtac a atgctAGTC |

WO 2005/002324 PCT/IB2004/002491

Figure 14 (a)

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201 PGI int U --->
                                                       25.0
 consePGIinTUNTDrakka
                        CTGT
                             CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
        consensWesrPGI
                        CTGT
                             CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
                        CTGT
    consePGIintUNTR113
                             CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
 consePGIintUNTBrapaA
                        CTGT
                             CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
   ConsePGIintUNTRRH1
                        CTGT
                             CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
                        CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
    PGIBO-EM: AF258277
                        CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
   PGIBra-EM: AF258278
                        CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
 consePGIintUNTBolera
                        CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
  consePGIintUNTR2000
            Consensus
                        ctgtcagcac taatcttgc ggtatg aatt tgtgattaaa tttgtttgt
 consePGIinTUNTDrakka
                        TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
       consensWesrPGI
                       TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
                        TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ...AATGTATA
   consePGIintUNTR113
                        TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ...AATGTATA
 consePGIintUNTBrapaA
   ConsePGIintUNTRRH1
                        TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
    PGIBO-EM: AF258277
                       TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
                       TGTGACTCTT TTCTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
   PGIBra-EM: AF258278
 consePGIintUNTBolera
                       TG.GACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
                       TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
  consePGIintUNTR2000
                       tg.gactctt t.cttcattg ttcgttttcg tacaataaac cgaatgtata
            Consensus
                        301
                                                       PGIol antL 341
                                                                             350
                       ATCTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
 consePGIinTUNTDrakka
                       ATCTTTTAC AAACTGAA IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
       consensWesrPGI
   consePGIintUNTR113
                       ATCTTTTAC AAACTGAA IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
                       ATCTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBrapaA
                       ATCTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
  ConsePGIintUNTRRH1
   PGIBo-EM: AF258277
                       ATCTTTTAC AAACTGAA IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
                       ACCTTTTAC AAACTGAA AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC
  PGIBra-EM: AF258278
consePGIintUNTBolera
                       ATCTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
 consePGIintUNTR2000
                       ATCTTTT.AC AAACTGAA IT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
          Consensus
                      atctttttac aaactgaa tt ttctaccggg tctgatgtac a atgctAGTC
                       351
consePGIinTUNTDrakka
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CT.CATGTAT TCAGACAGTA
      consensWesrPGI
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
  consePGlintUNTR113
consePGIintUNTBrapaA
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
  ConsePGIintUNTRRH1
   PGIBo-EM: AF258277
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
  PGIBra-EM: AF258278
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
consePGIintUNTBolera
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
                       TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
 consePGIintUNTR2000
                      TCCATGTTCT TGGGGATCAT GATTTATTTT CTaCATGTAT TCAGACAGTA
           Consensus
                                                                           450
consePGIinTUNTDrakka
                      CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
                       CAGAAGAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
      consensWesrPGI
                      CAGAAGAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
 consePGIintUNTR113
                      CAGAAGAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTBrapaA
                      CAGAAGAAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
  ConsePGIintUNTRRH1
                      CAGAAGAAG TATTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
   PGIBO-EM: AF258277
                      CAGAAGAAA TGTTTAAAAC TCTGGATGTT TTGATTTACA GTTAGTGGAG
 PGIBra-EM:AF258278
                      CAGAAGAAAG TGTT AAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTBolera
                      CAGAAGAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
CAGAAGAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTR2000
           Consensus
```

Figure 14 (b)

| | • | | | | | |
|---|--|-------------------|--|---|------------------------|---|
| | | 451 | | ata Base PG | | . 500 |
| | consePGIinTUNTDrakka | | | A CAATGCATTI | | |
| | consensWesrPGI | | | A CAATGCATTI | | |
| | consePGIintUNTR113 | | | A CAATGCATTI | | |
| | consePGIintUNTBrapaA | | | A CAATGCATTI | | |
| | ConsePGIintUNTRRH1 | | | A CAATGCATTI | | |
| | PGIBO-EM:AF258277 | AAGTTCGGC | A TTGATCC | | •••••• | • |
| | PGIBra-EM: AF258278 | | | A CAA | | |
| | consePGIintUNTBolera | | | A CAATGCATTT | | |
| | consePGIintUNTR2000 | | | A CAATGCATTT | | |
| | Consensus | AAGTTCGGCA | 1 TIGATCCga | a caatgcattt | gcatttggg | actgggttgg |
| | | 501 | | | | 550 |
| | consePGIinTUNTDrakka | | | r GCTTGTTTAT | mmccmmcm x m | |
| | | | | • | | |
| | consensWesrPGI | | | GCTTGTTTAT | | AATTTCTCG |
| | consePGIIntUNTR113 | | | GCTTGTTTAT GCTTGTTTAT | | |
| | consePGIintUNTBrapaA ConsePGIintUNTRRH1 | • | | GCTTGTTTAT | | |
| | PGIBO-EM: AF258277 | | | GCIIGIIIAI | | |
| | PGIBra-EM: AF258277 | • | | • | | |
| | consePGlintUNTBolera | | | GCTTGTTTAT | | മിമ മത്ത്യവാദ് |
| | consePGIintUNTR2000 | | | GCTTGTTTAT | | |
| | | | | gcttgtttat | | |
| | Consensus | tggaaggtac | agrggraagi | . gettyttat | ttggttgtat | [Jaattectq.] |
| | | 551 | • | | | 600 |
| | consePGlinTUNTDrakka | | י רייירבריייזביי | GTATAACTGA | እ አ ጥጥ ር ተመቀጥጥር | |
| , | consensWesrPGI | | | GTATAACTGA | | |
| | consePGIintUNTR113 | | | TTATAACTGA | * | |
| | consePGIintUNTBrapaA | | and the second s | TTATAACTGA | -,, | |
| • | ConsePGIintUNTRRH1 | | | TTATAACTGA | | |
| | PGIBO-EM: AF258277 | | | • | | |
| | PGIBra-EM: AF258278 | | | | •••• | |
| • | consePGIintUNTBolera | TCCATTTCCG | CTTGCTTAGT | GTATAACTGA | AATTCTTTTG | CAGTTTGCAG |
| | consePGIintUNTR2000 | TCCATTTCCG | CTTGCTTAGT | GIATAACTGA | AATTCTTTTG | CAGTTTGCAG |
| | Consensus | tccathtccg | cttgcttagt | tataactga | aattcttttg | cagtttgcag |
| | | 10 | | ii | | • |
| | • | 601 | | transfer of the second | | 650 |
| c | onsePGlinTUNTDrakka | TGCTGTTGGA | GTCTTACCAT | TGTCTCTACA | GTATGGCTTC | TOTGTGGTTG |
| | consensWesrPGI | TGCTGTTGGA | GTCTTACCAT | TGTCTCTACA | GTATGGCTTC | TOTGTGGTTG |
| | consePGIintUNTR113 | | | TGTCTCTACA | | |
| C | onsePGIintUNTBrapaA | TGCTGTTGGA | GTCTTACCAT | TGTCTCTACA | GTATGGCTTC | TCCGTGGTTG |
| | ConsePGIintUNTRRH1 | TGCTGTTGGA | GTCTTACCAT | TGTCTCTACA | GTATGGCTTC | TCCGTGGTTG |
| | PGIBo-EM: AF258277 | • • • • • • • • • | • | • • • • • • • • • | • • • • • • • • • | |
| | PGIBra-EM: AF258278 | | | | | |
| | onsePGIintUNTBolera | | | TGTCTCTACA | | = |
| | consePGIintUNTR2000 | | | TGTCTCTACA | | Hed |
| | Consensus | tgctgttgga | gtcttaccat | tgtctctaca | gtatggcttc : | |
| | | | • | | | 12 |
| | | 651 | | _ | | 700 |
| C | onsePGIinTUNTDrakka | | | TTTATCAGCC | | |
| | consensWesrPGI | | | TTTATCAGCC | | |
| | consePGIintUNTR113 | | | TTTATTAGCC | | |
| C | onsePGIintUNTBrapaA | | | TTTATTAGCC A | | |
| | ConsePGIintUNTRRH1 | | | TTTATTAGCC A | | |
| | PGIBO-EM: AF258277 | | • | ••••• | • | |
| _ | PGIBra-EM: AF258278 | | | | | |
| | onsePGIintUNTBolera | | | TTTATGAGCC . | | |
| • | consePGIintUNTR2000 | | | TTTATEAGCC | | |
| | Consensus | agaagtacgg | taccttctac | tttat Jagoc | atctcataaa a | |
| | • | | | 13 | | 14 |

Figure 14 (c)

| | ; | | | • | |
|----------------------|---|-------------|---|---|-------------------|
| • | 701 | • | · · · · <u>-</u> | | 750 |
| consePGIinTUNTDrakk | | | TTCCTCT[]A | | |
| consensWesrPG: | I CATATTCTT | T CTATTTAT | T TTCCTCT[A | A TGATTTCTTC | TITTTTTA |
| consePGIintUNTR11: | 3 CATATTCT | T CTATTTAT | T TTCCTCTGA | A TGATTTCTTC | TCTTTTAT |
| consePGIintUNTBrapa/ | A CATATTCTT | T CTATTTAT | T TTCCTCTGAZ | TGATTTCTTC | TCTTTTAT |
| ConsePGIintUNTRRHI | | | T TTCCTCTGA | | |
| PGIBO-EM: AF258277 | | | | | |
| PGIBra-EM:AF258278 | | | | • | |
| consePGIintUNTBolera | | ጥ ሲጥውጥ ልጥ | T TTCCTCTTAX | , mc/mmmcmmc | الاستستستالي |
| consePGIintUNTR2000 | | | | | |
| | | | T TCCCTCTIAZ | | |
| Consensus | catattett | t ctatttat | t ttcctct.aa | tgatttcttc | |
| | 1_ | 4.5 | 15 | | . 16 17 |
| | 751 | | | • | 800 |
| consePGIinTUNTDrakka | | | C AAAAGTTGTT | | |
| consensWesrPGI | | | C AAAAGTTGTT | | |
| consePGIintUNTR113 | | | C AAAAGTTGTC | | |
| consePGIintUNTBrapaA | | | C AAAAGTTGTC | | |
| ConsePGIintUNTRRH1 | TGCATTCCC | G TTTTATTTT | C AAAAGTTGTC | ACTGTCTCTA | AATCAAGAAG |
| PGIBO-EM: AF258277 | | | | | |
| PGIBra-EM: AF258278 | | | | | |
| consePGIintUNTBolera | TGCATTCCC | TTTTATTT. (| CAAAAGTTGTC | CGGCCCCCTA | AACCAAGAAG |
| consePGIintUNTR2000 | | | C AAAAGTTGTT | | |
| Consensus | tgcattccc | ; ttttatttt | aaaagttgt. | actgtctcta | aatcaagaag |
| | | • | • • • | | |
| | 801 | . * | • | · · · | 850 |
| consePGIinTUNTDrakka | AAACCTTCTT | AGTAGATCC | GOTGATATTC | AGCCTTTTTT | AAATTGGACT |
| consensWesrPGI | AAACCTTCTT | AGTAGATCC | GTGATATTC | AGCCTTTTTTT | AAATTGGACT |
| consePGIintUNTR113 | | | GTTGATATTC | | |
| consePGIintUNTBrapaA | AAACCTTCTT | AGTAGATCCA | G.TGATATTC | AGCCTTTTCT | AAATTGGACT |
| ConsePGIintUNTRRH1 | | | GTTGATATTC | | |
| PGIBo-EM: AF258277 | | | • • • • • • • • • • | | |
| PGIBra-EM: AF258278 | | | ••••• | | |
| consePGIintUNTBolera | AAACCTTTCT | AGGACCA | GACTCC | | AAATTGGACT |
| consePGIintUNTR2000 | | | GTGATATTC | | |
| Consensus | | | g.tgatattc | | |
| | | uguuguuuu | 18 | 19 | daactggact |
| | 851 | | | 4 2. | 900 |
| consePGIinTUNTDrakka | | אאא פפנאפר | TTCAAGCATT | CATALACCATT | |
| consensWesrPGI | | | TTCAAGCATT | | TCCAGTCCAC |
| consePGIintUNTR113 | | | TTCAAGCATT | | |
| consePGIintUNTBrapaA | | | TTCAAGCATT | | |
| ConserGlintUNTRRH1 | | 4.4 | TTCAAGCATT | | |
| PGIBO-EM: AF258277 | GCAGGIIIII | | | GATCAGCATT | ICCAGICCAC |
| PGIBra-EM: AF258278 | • | •,••••• | • | • | • • • • • • • • • |
| | CONCOMMEN | *** 000000 | MMCP PCCPMM | camba coama | |
| consePGIintUNTBolera | | | TTCAAGCATT | | |
| consePGlintUNTR2000 | | | TTCAAGCATT | | |
| Consensus | gcaggttttt | aaa.gggagc | ttcaagcatt | gati agcatt (| tccagtcc.c |
| | | • | | 20 | |
| | 901 | | | | 950 |
| consePGIinTUNTDrakka | | | CCCGTGAGTT | | |
| consensWesrPGI | | | CCCGTGAGTT | | |
| consePGIintUNTR113 | | | CCCGTGAGTT (| | |
| consePGIintUNTBrapaA | . CCCGTTTGA | GAAGAATATA | CCCGTGAGTT (| GCATTAGTT. G | TGTGATTAT |
| ConsePGIintUNTRRH1 | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT (| GCATTAGTT. G | TGTGATTAT |
| PGIBo-EM: AF258277 | • | | | | • • • • • • • • |
| PGIBra-EM: AF258278 | | | | | |
| consePGIintUNTBolera | | | CCCGTGAGTT (| | |
| consePGIintUNTR2000 | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT (| GCATTAGTT. G | TGTGATTAT |
| Consensus | acc.gtttga | gaagaatata | cccgtgagtt q | gcattagtt. g | tgtgattat |
| | - | · . | | | |

Figure 14 (d)

| | | | | • | • | | |
|---|----------------------|-------------------|------------|---|--------------|-------------------|---|
| | | 951 | | | | . 1 <u>0</u> 00 | |
| | consePGIinTUNTDrakka | ACAGTTTTTC | TTGTCTTTTT | GCTATGCCCA | TCAACACTAG | AAGATTOGTG | |
| | . consenswesrPGI | | TTGTCTTTT. | | | | |
| | consePGIintUNTR113 | ACAGTTTT.C | TTGCCTTTTT | GCTAT AGG | GCAAC.CTAG | A.GATTCATG | |
| | consePGIintUNTBrapaA | | TIGICITIT. | | | | |
| | ConsePGIIntUNTRRH1 | | TTGTCTTTTT | | | | |
| | PGIBO-EM: AF258277 | | | | | | |
| • | PGIBra-EM: AF258278 | | 1.4.4. | | | | |
| | consePGIintUNTBolera | ል ርልርጥጥጥ ር | TTGTCTTTTT | GCTAG. TGA | TCAAC . CTAG | A.GATTCGTG | |
| | | | TTGTCTTTTT | | | | |
| | consePGIintUNTR2000 | | | | | | |
| | Consensus | acagttt.c | ttgtctttt | gctata | ccaac.ccay | 21 | |
| | | | • | | | 21 | |
| | | | • | | • | • | |
| | | 1001 | • | | | 1050 | |
| | consePGIinTUNTDrakka | AAGTTATTAG | TGTAGCCAAC | GCCTAGGGGG | AGGTTGGTTG | GCTGTTTTGG | , |
| | consensWesrPGI | AAGTTATTAG | TGTAGTCAAC | GCA | | • • • • • • • • • | |
| • | consePGIintUNTR113 | | TGTAGTCAAC | | | | |
| | consePGIintUNTBrapaA | AAGTTATTAG | TGTAGTCAAC | GCAGAGTGAG | AGG. TGATTG | | |
| , | ConsePGIintUNTRRH1 | AAGTTATTAG | TGTAGTCAAC | GCAGAGGAGG | AGATGGTT | • • • • • • • • | |
| | PGIBO-EM: AF258277 | | | | | | |
| | PGIBra-EM: AF258278 | | | | | | |
| | consePGIintUNTBolera | | TGTAGTCAAC | | | | |
| | consePGIintUNTR2000 | | TGTAGTCAAC | | | | |
| | Consensus | aagttattag | tgtagtcaac | gca.agg.g. | .g | •••••• | |
| | | | | | | | |
| | | 1051 | • | 1076 | | 100 LL 12 | |
| | consePGIinTUNTDrakka | ACGTTTTCAC | GTGCTCCGGG | | | CCCAAC | |
| | consensWesrPGI | | | ••••• | | • • • • • | |
| | consePGlintUNTR113 | | | | | •••• | |
| | consePGIintUNTBrapaA | | | • • • • • • • • • | | • • • • • | |
| | ConsePGIIntUNTRRH1 | • • • • • • • • • | ••••• | • | | | |
| | PGIBO-EM: AF258277 | | | | | •••• | |
| | PGIBra-EM: AF258278 | | | • • • • • • • • | | ••••• | |
| | consePGIintUNTBolera | | | | | | |
| | consePGIintUNTR2000 | ACGATTTCAG | GTGCTTTAGG | GTTATTG | | •••• | |
| | | | | | | | |

Figure 15 (a)

| | 51 | 100 |
|---|---|---|
| EMBH44836anti | | |
| GCP18-5CP418L-Sams | | |
| GCP18-2CP418L-Wes | | |
| GCP18-4CP418L-R2000 | | CP418L |
| consel29bal-Drak | | AAATTCTAAA TTTCTCCA |
| | AAAC TATGTA ACAAAAATCA | AAATTGTAAA TGTCTCCA |
| GCPS18-129Sam-ba2 | AMMC INIGIA ACAMANATOR | AAATTGTAAA TGTTCCCT. |
| GCPR18-3129R211-ba2 | | |
| GCP18-10129R20-ba2 | | AAATTGTAAA TGTC.CCT |
| Consensus | | •••••• |
| | | 150 |
| | 101 | , |
| EMBH44836anti | ************************************** | A.CATTTTCT GTAA |
| GCP18-5CP418L-Sams | | |
| GCP18-2CP418L-Wes | | |
| GCP18-4CP418L-R2000 | | |
| consel29bal-Drak | TCACAAGGAC CTACAGAATA GAGTTATCAT | |
| GCPS18-129Sam-ba2 | TOGTANGENC . TACAGANTA GAGTTATCA | r AACATTICI G AA |
| GCPR18-3129R211-ba2 | TEGTAACGEC CTCAAAAA.A GAGGTATCA | AAC. TTITCT GT.A |
| GCP18-10129R20-ba2 | TESTTACCC C.CAAAAA.A AAGGTCA | A AACTT.TCCG GTAA |
| Consensus | | |
| | | 200 |
| · | 151 | 200 |
| EMBH44836anti | TATTTCCAT CAAAATGA CTAGAGAAC | AGCAGITCIT ATAACATTAT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes | TATTTCCAT CAAAATGA CTAGAGAAC | AG.AGTICIT ATAACATIAT |
| GCP18-4CP418L-R2000 | ATATTTCCAT CAAAATGACTAGAGAAC | AG.AGITCTT ATAACATTAT |
| consel29bal-Drak | | AG.AGITCTT ATAACATTAT |
| GCPS18-129Sam-ba2 | | ATAATTAAT ATA.CATTIT |
| GCPR18-3129R211-ba2 | ATGTTTCCAT CAAAATG. CTATCGGAC | ATANTANT ATANC.TTCT |
| GCP18-10129R20-ba2 Consensus | ATGTITCCAT CANALIG. CITCGGA.C | ATAATTAAA ACATTCT |
| CONSCIPERS | MIGILIACOL CLASSICA CONTRACTOR | |
| | ** The second of the second of | |
| | 201 | 250 |
| EMBH44836anti | | |
| EMBH44836anti GCP18-5CP418L-Sams | CTGTAAA TG.TTCCAA CAAAA CCACT AC | ATAGCAGAGTTC .TTATAACAT |
| | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC | TADACAGATTC .TTATAACAT TADACAGATTC ATTATAACAT |
| GCP18-5CP418L-Sams | CTGTARA TG.TTCCAR CARRA CCACT AC CTGTARA TG.TTCCAR CARRA CCACT AC CTGTARA TG.TTCCAR CARRA CCACT AC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak | CTGTARA TG.TTCCAR CARRA CCACT AC CTGTARA TG.TTCCAR CARRA CCACT AC CTGTARA TG.TTCCAR CARRA CCACT AC CTGTARA TG.TTCCAR CARRA CCACT AC | TATAACAT. TATAACAT TATAACAT TATAACAT TATAACAT TATAACAT TATAACAT TATAACAT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 | CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTG.RARATARTTCCCCTCARARATTR | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCCTCAAAAATTAC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTAGAAAAA ATTTTCTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129ba1-Drak GCPS18-129Sam-ba2 | CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTGTARA TG.TTCCAR CARAR CCACT AC CTG.RARATARTTCCCCTCARARATTR | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTAGAAAAA ATTTTCTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129ba1-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCCTCAAAAATTAC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTAGAAAAA ATTTTCTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129ba1-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 | CTGTARA TG.TTCCAR CARRA CCACT AC CTG.RARATATTCCCTCARARATTR | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TTAGAA.A. ATT TTC T.AGAA.A. ATT TTC T.AGAA.A. |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCCTCAAAAATTAC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TTAGAA.A. ATT TTC T.AGAA.A. |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129ba1-Drak GCP518-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAAT.ATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TTAGAA.A. ATT TTC T.AGAA.A. ATT TTC T.AGAA.A. ATT. TTC T.AGAA.A. 300 .CTATACC |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129ba1-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAATAATTCCCTCAAAAATTAAC CTG.AAAA.TAATTCCCTCAAAATTAAC CTG.AAA.TAATTCCCTCAAAATTAAC CTG.AAAA.TAATTCCCTCAAAATTAAC CTG.AAAA.TAATTCCCTCAAAATTAAC CTG.AAAA.TAATTCCCTCAAAATTAAC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .T.ACAA.A. AT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAATAATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC CTG.AAA TAATTCCCT CAAAA TTAAC CTG.AAA ATATTCCCT CAAAA TTAAC TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT .TTC .TTATAACAT ATTATAACAT CAGAACAAAG .CTCCTATAAC CAGAACAAAG .CTCCTATAAC |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP718-3129R211-ba2 GCP718-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAAT.ATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTAGAA.A. AT TTC .T.AGAA.A. 300 .CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAATAATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC CTG.TGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TAGAA.A. AT. TTC T.ACAA.A. 300 .CTATACC CAGAACAAAG CTCCTATAAC |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCTCAAAAATTAC CTG.AAAATAATTCCCT CAAAA TTAAC CTG.AAA.TAATTCCCT CAAAA TTAAC CTG.TGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TAGAA.A. AT. TTC T.ACAA.A. 300 .CTATACC CAGAACAAAG CTCCTATAAC |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCPR18-3129R211-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTACAA.A.A. ATT TTC T.ACAA.A. ATT TTC T.ACAA.A. ATT TTC T.ACAA.A. CAGAACAAAG CTCCTATAAC CATCAAAAG AGACTCCA.G |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCPR18-10129R20-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC TGTTTC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .T.ACAA.A.A. TTC .T.ACAA.A.A. 300 .CTATACC .CAGAACAAAG .CAGAACAAAG .CAGAACAAAG .CAGAACAAAG .CATCAAAAATG .CATCAAAAATG .CATCAAAATG .CATCAAAATG .CATCAAAATG .CATCAAAATTG .GACTCAA.G.G .CATCAAAATTG .GACTCAA.G.G .CATCAAAATTG .GACTCAA.G.G .CATCAAAATTG .GACTCAA.G.G |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCPR18-3129R211-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT .TTC .TTATAACAT .TTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ACAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCPR18-10129R20-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC TGTTTC | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT .TTC .TTATAACAT .TTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ACAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCPR18-10129R20-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT ACCTGTAAA TG.TTCCAA CAAAA CCACT ACCTGTAAA TG.TTCCAA CAAAA CCACT ACCTGTAAA TG.TTCCAA CAAAA CCACT ACCTG.AAAATAATTCCCT CAAAA TTA. CCTG.AAAATAATTCCCT CAAAA TTA. ACCTG.AAAA.TAATTCCCT CAAAA TTA. ACCTG.AAAA.TAATTCCCT CAAAA TTA. ACCTG.AAAA.TAATTCCCT CAAAA TTA. ACCTG.AAAA.TAATTCCCT CAAAA TTA. ACCTGTCTGT.AA ATGTCCAATC AAAACCACTATGTCTGT.AA ATGTCCAATC AAAACCACTATGTCTGT.AA ATGTCCAATC AAAACCACTATGTTTCC. TGTTTC. TGTTTC. tttctgt.aa tgtttccatc aaaatgacta | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT ATT TTC .TTATAACAT .TTC .TTATAACAT .TTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ATTC .TTATAACA.A.ACAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CAGAACAAAG .CTCCTATAAC .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G .CATCAAAAATG .AGACTACA.G |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP718-3129R211-ba2 GCP718-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-5CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP718-3129R211-ba2 GCP718-10129R20-ba2 Consensus | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC. TGTTTC. TGTTTC. tttctgt.aa tgtttccatc aaaatgacta | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TTACAA.A. AT TTC T.ACAA.A. AT TTC T.ACAA.A. 300 CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG AGACTACA.G CATCAAAATG AGACTACA.G tcgaacataa ttaatataac |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCPR18-3129R211-ba2 GCPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTAC CTG.AAAAT.ATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC 251 TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC TGTTTC TGTTTC TGTTTC TGTTTC TGTTTC TGTTTC TTGTTTC TTGTTTT ATACAAAGTT TCACT AAA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATT TTC TTAGAA.A. ATT TTC TTAGAA.A. TTC T.ACAA.A. 300 .CTATACC .CAGAACAAAG CTCCTATAAC .CAGAACAAAG CTCCTATAAC .CAGAACAAAG CTCCTATAAC .CAGAACAAAG CTCCTATAAC .CAGAACAAAG CTCCTATAAC .CATCAAAATG ACACTAGA.G .CATCAAAACTT CCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA | ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTATAACAT ATAGCAGAGTTC .TTAGAA.A.A. ATT |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-10129R20-ba2 CONSENSUS | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT.CAAAAATTAC CTG.AAAATAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATT TTC TTAGAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. 300 CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG CTCCTATAAC CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-10129R20-ba2 Consensus | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT.CAAAAATTAC CTG.AAAATAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATT TTC TTAGAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. 300 CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG CTCCTATAAC CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG AGACTAGA.G CATCAAAATG TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-4CP418L-R2000 consel29bal-Drak | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT.CAAAAATTAC CTG.AAAATAATTCCCT.CAAAA TTAAC CTG.AAAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC CTG.AAA.TAATTCCCT.CAAAA TTAAC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATAGCAGAGTTC TTAGAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. 300 CATATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG AGACTCGA.G CATCAAAATG AGACTCGA.G CATCAAAATG AGACTAGA.G CATCAAAATG TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 GCP618-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCP18-4CP418L-R2000 conse129bal-Drak GCP18-4CP418L-R2000 conse129bal-Drak GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC. TGTTTC. TGTTTC. TGTTTC. TGTTTC. TTGTTTT ATACAAAGTT TCACT AAA A TTGTTT ATACAAAGTT CACT AAA A TTGTTT ATACAAAGTT TCACT AAA A TTGTTT ATACAAAGTT TCACT AAA A TGTTT ATACAAAGTT TCACT AAA ATGTTT ATACAAAGTT TCACT AAA ATGTTT ATACAAAGTT TCACT AAA ACC.CAGTTC THGCATAGTT TCACTTAAA | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATAGCAGAGTTC TTACAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. 300 CATATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG AGACTCAA.G CATCAAAATG AGACTACA.G CATCAAAATG AGACTACA.G TCTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 consel29bal-Drak GCPS18-129Sam-ba2 GCPR18-3129R211-ba2 GCPR18-3129R211-ba2 GCPS18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCPS18-10129R20-ba2 Consensus GCPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC. TGTTTC. TGTTTC. TGTTTC. TTGTTTC. TTGTTTT ATACAAAGTT TCACT AAA A TTGTTT ATACAAAGTT TCACT AAA AC.CAGTTC TIGCATTAGT TCACT.AAA ACC.CAGTTC TIGCATTAGT TCACT.AAA ACC.CAGTTC TIGCATTAGT TCACT.AAA ACC.CAGTTC TIGCATTAGT TCACT.AAA | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATT TTC TTACAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. GOOD CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG AGACTCA.G CATCAAAATG AGACTCA.G CATCAAAATG AGACTACA.G TCTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |
| GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 GCP18-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 GCP618-3129R211-ba2 GCP18-10129R20-ba2 Consensus EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Sams GCP18-4CP418L-R2000 conse129bal-Drak GCP18-4CP418L-R2000 conse129bal-Drak GCP18-4CP418L-R2000 conse129bal-Drak GCP518-129Sam-ba2 | CTGTAAA TG.TTCCAA CAAAA CCACT AC CTG.AAAATAATTCCCT CAAAA TTA. AC CTG.AAAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC CTG.AAA.TAATTCCCT CAAAA TTA. AC TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTCTGT.AA ATGTCCAATC AAAACCACTA TGTTTC. TGTTTC. TGTTTC. TGTTTC. TGTTTC. TTGTTTT ATACAAAGTT TCACT AAA A TTGTTT ATACAAAGTT CACT AAA A TTGTTT ATACAAAGTT TCACT AAA A TTGTTT ATACAAAGTT TCACT AAA A TGTTT ATACAAAGTT TCACT AAA ATGTTT ATACAAAGTT TCACT AAA ATGTTT ATACAAAGTT TCACT AAA ACC.CAGTTC THGCATAGTT TCACTTAAA | ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC ATTATAACAT ATAGCAGAGTTC TTATAACAT ATT TTC TTACAA.A. ATT TTC T.ACAA.A. AT. TTC T.ACAA.A. GOOD CTATACC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CAGAACAAAG CTCCTATAAC CATCAAAATG AGACTCA.G CATCAAAATG AGACTCA.G CATCAAAATG AGACTACA.G TCTACAAACTT TCCCCGTAAA T CTACAAACTT TCCCCGTAAA |

Figure 15 (b)

| | 351 | | • | | 400 |
|---|-------------|---|---------------|--------------------------|--------------|
| | TGAGCTTAAT | ATCACCCAA. | GATGTTTCA | ATCAGAT AAA | GAGTAACGAC |
| EMBH44836anti | TGAGCTTAAT | ATCACCCAAA | GATGTTTCA | ATCAGAT AAA | GAGTAACGAC |
| GCP18-5CP418L-Sams | TGAGCTTAAT | ATCACCCADA. | GATGTTTCA | ATCAGAT AAA | GAGTAACGAC |
| GCP18-2CP418L-Wes | TGAGCTTAAT | MICHCCCHAI | GATGTTTCA | ATCAGAT AAA | GAGTAACGAC |
| GCP18-4CP418L-R2000 | TGAGCTTAAT | MICHCCCHAR | CATCTTTCA | ATCAGAT AAA | GAGTA . CGAC |
| consel29bal-Drak | TGAGCTTAAT | ATCACCCAAA | C MEDICAG | атсафат фаа | GN |
| GCPS18-129Sam-ba2 | TAA | | G. TITALLAU | ATCACAT GAA | Co |
| GCPR18-3129R211-ba2 | AAT | CITATIONA. | | ATCACAT GA | 6/ |
| GCP18-10129R20-ba2 | TAA | CHIRITOTIAAA | G. TITATICAC | ATCACAT GAA | GAL |
| Consensus | | | | | |
| Consenada | • | | | | |
| • | 401 | • | | | • • |
| EMBH44836anti | ATCGTTTTGA | GATTAGAACA | AA . | | * |
| GCP18-5CP418L-Sams | ATCGTTTTGA | GATTAGAACA | AA | | |
| | ATCGTTTTGA | CATTAGAACA | AA | | |
| GCP18-2CP418L-Wes | ATCGTTTTGA | GATTAGAACA | AA | | |
| GCP18-4CP418L-R2000 | ATCGTTTTGA | CATTAGAACA | AA | | |
| consel29bal-Drak | ATCGTTTTGA | GACC | 22 | | |
| GCPS18-129Sam-ba2 | | | 22. | | |
| GCPR18-3129R211-ba2 | | | AA | | |
| GCP18-10129R20-ba2 | | <u>g</u> GC | A. | | |
| Consensus | | · | | | 480 |
| 00,20,00 | 431 | 2 | | , | |
| EMBH44836anti | | CGTAGAGTGA | TTTGAGGAGT | AGGCTCGTTG | CCAGCAGAGU |
| GCP18-5CP418L-Sams | | ころ これ | TTTCACCACT | AGGCTCGTTG | CCAGCAGAGC |
| GCD18-2CD4101-3am3 | | ここの これ これ これ これ これ | TTTGAGGAGT | AGGCTCGTTG | CCAGCAGAG. |
| GCP18-2CP418L-Wes | | へつかり こり こかこう | TTTCACCACT | AGGCTCGTTG | CCAGCAGAGC |
| GCP18-4CP418L-R2000 | | COMMONCACTOR | THENCIAGE | AGGCTCGTTG | CAGCAGAGC |
| consel29bal-Drak | | COURSE OF CALCAR | THYCAGGAGT | AGGCTCGTIG | CCAGCIGGAGG |
| GCPS18-129Sam-ba2 | GIMAAGCIIA | COLNOROTOR | TOTOLOGICA | AGGCTCGTTG | CCAGCGGAGC |
| GCPR18-3129R211-ba2 | GTAAACCTTA | GGTAGAGTGA | - ICI GAGGAGI | ACCCTCCTTG | CCACCIGGAGC |
| GCP18-10129R20-ba2 | GTAA. CCTTA | ddragagrga | TUIGAGGAGI | AGGCTCGTTG | CORC GROC |
| Consensus | .t.aa.ctta | c.tagagtga | t.tgaggagt | aggctcgttg | ccage.g-g- |
| | | ٠. | • | | 530 |
| | 481 | | | CMMCC & CCTG | |
| EMBH44836anti | TAGCTCTCTC | CTCCGCCTCA | TGAAGCATCT | GTTGCACCTG | ACACAACCGT |
| GCP18-5CP418L-Sams | TAGCTCTCTC | CTCCGCCTCA | TGAAGCATCT | GTTGCACCTG | AGACAACCGT |
| GCP18-2CP418L-Wes | TAGCTCTCTC | CTCCGCCTCA | TGAAGCATCT | GTTGCACCTG | ACACAACCGT |
| GCP18-4CP418L-R2000 | TAGCTCTCTC | CTCCGCCTCA | TGAAGCATCT | GTTGCACCTG | ACACAACCGT |
| consel29bal-Drak | TAGCTCTCTC | CTCCGCCTCA | TGAAGCATCT | GTTGCACCTG | ACACAACCCT |
| GCPS18-129Sam-ba2 | TAGCTCTCTC | CTCC.CCTCA | TGAAGCATCT | GGTGCACCTG | AGACAACCGI |
| GCPR18-3129R211-ba2 | | CTCCCCCCTCA | TGAAGCATCT | GCTGCACCTG | AGACAACCGI |
| GCP18-10129R20-ba2 | | とからし こうしゅうしょう | TGAAGCATCT | GOTGUACUTG | MGWCW - CCC- |
| | tagetetete | ctccacctca | tgaagcatct | g.tgcacctg | agacaaccgt |
| Consensus | Lagerere | CCCCGCCCC | | | |
| • | 631 | | | | 580 |
| | 531 | TOCATOACO | CCACCAGAA | TTCGACGCCG | CGCATCGGAA |
| EMBH44836anti | | | CCCACCAGAA | TTCGACGCCG | CGCWICGGG |
| GCP18-5CP418L-Sams | | | CCCACCAGA | TTCGALGCCG | COCK! COCK. |
| GCP18-2CP418L-Wes | | めっこことをしなって | CCCACCAGAA | TTCGACGCCG | COCHI COCHE. |
| GCP18-4CP418L-R2000 | | maacamcacc | CCC CCAGAA | TTCGALGULG | CGCWICGGRA |
| consel29bal-Drak | | | CCCACCAGAA | TTCGALGULG | CCCV1 CCCC |
| GCPS18-129Sam-ba2 | GACGAAACTT | TCCGATCACC | CCCACCAGAA. | TTCGACGCCG | CGCATCGGAA |
| GCPR18-3129R211-ba2 | GACGAAACTT | TCCGATCACC | CCC CCAGAA | TTCGACGCCG | CGCATCGGAA |
| GCP18-10129R20-ba2 | GACGAAACTT | TCCGATCCCC | -conconcon | ttcgacgccg | cacatcagaa |
| Consensus | gacgaaactt | tecgateace | gccaccagaa | cccgaogoog | |
| • | | • | | | 630 |
| | 581 | | > CMC3 3 CCCC | ACCEATOCOG | GGAGTGCGAC |
| EMBH44836anti | GGATCCGAAT | CGGGAACTGG | WEI GWYCCCG | AGCGATCCCG AGCGATCCCG | GGAGTGCGAC |
| GCP18-5CP418L-Sams | GGATCCGAAT | CGGGAACTGG | AGTGAACCCG | ACCCA PCCCC | GGAGTGCGAC |
| GCP18-2CP418L-Wes | GGATCCGAAT | CGGGAACTGG | AGTGAACCCG | AGCGATCCCG | GGAGTGCGAC |
| GCP18-4CP418L-R2000 | : _ | | プロサにア アレレル | AGCISATELEU | GOVERA |
| consel29bal-Drak | | へんぐんと かんかんじ | ACTGAACCCG | AGLIGATION | GGEGIOOTIO |
| GCPS18-129Sam-ba2 | | COCCA A CRCC | ካርጥርል ነርርነልር | AGCGATUCUL | GOMOIGCONG |
| | | COC BACECO | A CACO Y CLAR | AGCGATCCCG | GRAGIACONC |
| GCPR18-3129R211-ba2 GCP18-10129R20-ba2 | | CCCCA ACTGG | AGTGAACCIAIG | AGCGATCCCG | GCHGIGCGUC |
| | . GGMICCGMI | congrector | agtgaacc g | agcgatcccg | ggagtgcgaC |
| . Consensus | ggatccgaat | cyyyaactyy | | | ٠. |
| | | , , | • | | |

Figure 15 (c)

| | | • | | | |
|---------------------|--------------|------------|-------------|------------|--|
| • | 631 | • | | | 690 |
| EMBH44836anti | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT | TCGACGAAGA | GTGGAAGAGG |
| GCP18-5CP418L-Sams | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT | TCGACGAAGA | GTGGAAGAGG . |
| GCP18-2CP418L-Wes | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT | TCGACGAAGA | GTGGAAGAGG |
| GCP18-4CP418L-R2000 | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT | TCGACGAAGA | GTGGAAGAGG |
| consel29bal-Drak | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT | TCGACGAA.A | GTGGAAGAGG |
| GCPS18-129Sam-ba2 | GGAGCGTTGG | AAAAGAGAG | TGGCACGATT | TCGACGAAGA | GAGGAAGAGG |
| GCPR18-3129R211-ba2 | GGAGCGTTGG | AAAAAGAGAG | TGGCACGATT | TCGACGAAGA | GAGGAAGAGG |
| GCP18-10129R20-ba2 | GENECCHILGE | AAAAGAGAG | TGGCACGATT | TCG.CGAAGA | GAGGAAGAGG |
| Consensus | | _ | tggcacgatt | | |
| | | | | | |
| • | 691 | | | | 740 |
| EMBH44836anti | | | GCGTATGATC | | |
| GCP18-5CP418L-Sams | | | GCGTATGATC | | |
| GCP18-2CP418L-Wes | | | GCGTATGATC | | |
| GCP18-4CP418L-R2000 | | | GCGTATGATC | | |
| consel29bal-Drak | | | GCGTATGATC | - | |
| GCPS18-129Sam-ba2 | | | GCGTATGATC | | |
| GCPR18-3129R211-ba2 | | | GCGTATGATC | | |
| GCP18-10129R20-ba2 | | | GCGTATGATC | | |
| Consensus | agagggtggt | ggataaactc | gcgtatgatc | aagttcgtca | tcgtcctga. |
| | | • • | | | 700 |
| | 741 | | | | 29antiU 790 |
| EMBH44836anti | | | GGGCGCTCTG | | |
| GCP18-5CP418L-Sams | | | GGGCGCTCTG | | |
| GCP18-2CP418L-Wes | | | GGGCGCTCTG | | |
| GCP18-4CP418L-R2000 | | | GGGCGCTCTG | | , |
| consel29bal-Drak | | | GGGCGCTCTG | | |
| GCPS18-129Sam-ba2 | | | . GCCGCTCTG | | |
| GCPR18-3129R211-ba2 | TGCCGCC | | | | |
| GCP18-10129R20-ba2 | | | .GG.GCGCGG | | |
| Consensus | tgecgccat. | | .gg.gc.c.g | | • • • • • • • • • |
| | 791 | • | • | | • |
| EMBH44836anti | TCAATGAAC A | GTGACACGAC | GAAATGC | | |
| GCP18-5CP418L-Sams | TCAATGAAC A | | | | * * |
| GCP18-3CP418L-Sans | CCAATGAACA | | | | 14 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| GCP18-4CP418L-R2000 | CCAAIGAACA . | | | | • |
| consel29bal-Drak | | | | | |
| | | | | | , |

Figure 16

| Consen8C | 1 20 | 80 | 30 | 6 | 80 | 90 | 70 | 90 | 90 | 100 | 110 | 120 | 5 |
|---|--|----------------------------|------------|---------------------------------|--------------------------|---|-----------------|--|-----------------------|------------------------|--|--|---------------|
| Principaline Representine Principaline Principaline Principaline | TCTT GCARATATT GATCCTGTTGATG | ONTCCTATTO | | ВВАТАТСА ВТО | GACTANATCC | AGRARCTACTC | тяваттсят | TOCTRORRATATCHGTGGACTRAHTCCAGRAACTACTCTAGGTTCATGCTCARACTRTCARCARATT | САЯСЯВАТТ | CACTTTCAT | CACTITCATAGITICCATIGACGGATITICACIC | GREGGNITIT | |
| consend.olereceePGXU prinerPGXU Consensus | | | | | | | | | | | | | |
| FOOT STREET | 131 140 | 150 | 160 | 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 | C R O | |
| Atherpoline Principoline Principoline Principoline | GRCTANTICI GABGATACTI GIAATC | IGRTRCTTGTRI | | BBTOBTCTCOR | ABACGTTTAC | явсяостовяя | СЯЯТВСТТВ | RCATTGROGANTAGANTACARCAGCTGRARCRATGCTTARCGCCAGARCATTGROGARTGGGTAACAGCTCTTGGGTTAGATTACARCTGCTCTTGGGTTAGTATTCTGGGTTGGCATTGGGGGGGG | Танасанат | GGRTTRCRR GGRTRRCRG | ACATTGAGGRATTGGATTACAACTGCTCTTGGGTTAGTATCT ACATTGAGGGRATGGATAACAGCTGCTCTTGGGTTGGTATTT | BTTROTATET. | CT daca |
| consons, oteraceaplity | | | | | | | īd | pPGIoIU ^{ncm} | TGAGGAATT | ВОЯТТЯСЯВ | расяттоваяяттоомттясяястастсттоваттявтятст | GTTRGTATCT | |
| | 261 | 280 | 290 | 300 | 310 | 320 | | 340 | 010 | | | | : |
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| Conscient | | | | | | | 1CM1116 | | 133 | 151 | -caccTTaTT | COCCTTOTTOTG-TTACGRIGARIA | TGRATG |
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| consend.repaPOI prinerPGIIntU AthreenHJB21.12 | MACAGE AGE TETTA ACATGE GOTT AL | TINACATOTOS | TTRACT-RAC | RGGGCTCCGGC | ТОТТОСЯВЯ | ACT-ARCAGAGCTCCOUCTOTTACAAACATATAGGTTGCTG | | CACCACTANTET - 65 CONTAINS TO TOTAL OF THE T | STRICTED INTE | Ш | TTRRATTIG | 520 620 11101110000010 | 620 CGACTC |
| principilini Principilini concent olerant April principilini principilini | | TRACATG160 | TTRACTTARC | AGGGCTTCRGC AGGGCTCAGGC | TOTTGCAARA TOTTGCAAAA | ACT TANCAGGGCTT CRGCTOTTGCAARACATATGGTTGCTGT RCT TAACAGGGCTCAGGGCTGTTGCAAARACACATGGTTGCTGT | | ACTTARCHOGGETTCRGETOTTGCRARRCRIBTGGTTGCTGTCRGCRCTNDICTT-GEGOTATGCTR RETTARCHGGGETCRGGCTGTTGCRARRCRCRTGGTTGCTGTCHCHCHCTRATCTTTGCGGTATGHATTARAC | THIGHT | астнанатт | ATTTACTRARATTTCTTTTGGGGRCTTTDTTTCCTTRTT | ACTTTOTTTC | CTTATT |
| Consonate | | | | | | ··· PPGHn | H-J-Goncoc | OPC Hint Jasschaatste, gangtet | stets | : | | 11101116-68C1C | -GACTC |
| - | | 540 | 530 | 860 | 970 | 880 | 590 | 800 | 610 | 620 | S20 | | CROPE |
| ConsonB.repePGI | | | | | COTITICOINCRAIRBRC- | CRATRARC | -BR10 | TATARICT | TATARICITITIACABACTOR | TORNITTIC | 111TICTHECOGOTETION INTRA | Belgrada | 650 |
| Henfroganj821.12 prinorpGilect prinorantipGil | GTCCNTCTTAGTARACTTRARCTTCG | ARRETTARRET | | твсястсвявт | COTTCTORTT | АТОТЯВЯЯСЯ С | ятавсятат | IARCACATGCACTCGAGTCOTTCTGATTATGTAGAGAGAGATGACATGTTGATCCAGTCTTTTTAGARACTGA | гттявяяяс | | N. 1.A.T.CGRACRGRITTARI 160HQTRTGGTRGT | RR1GGRCTRT | GGTAGT |
| ConsonB.oleracoePGI | TTCTTCATTGT | ļ | | | ССТТТССТВ | ССТТТССТАСВАТАВАСССВЯТС | нте | TRTRATCT | TATARTCTTTTTACRARCTOR | TORNITIE | 11TICTRCCGGGTCTGAIGTRCA | GATGTACA | TOOL |
| Consenses | | | | | | | | | | tt.to | 3 - C - C - | toota or | |
| | | 670 | 089 | 690 | 700 | 710 | 720 | 230 | 740 |) B | 760 |) å | 700 |
| oonsoou.ropeful princepuljei Athropouljei princepuljei | CICCATGITCTTGGGGATCATGATTT CICGATGTTCTAGGA-AITATGATTT | IGGGATCATGA IGA-ATTATGA | | CCTCCTTCTAC | TCTACATGT | TTCRGCCRGTF TTCRGRCRGTF | CRGREGARG | NITITCTACATGI | CTBBATGTT | TARATTIBE | RGTTAGTGGA | ЗАНОТ ТСОСС | ATTONT |
| princent ipgil consens.oloracentus Consensus | CTCCATGTTCT | тасаалтсптая | | TCTRCNTGT | .ntgt | ттсявясявт | сявяявяя | ATTCAGACAGTÁCAGAAGAAAGAAAGTOTTCAAAACTCTGGATGTTTTAATTTACAGTTAGTGGAGAAGATTCGGCATTGAT | ICT GGATGTT | ттваттяс | ASTTOGIGGA: | omas I I I I I I I I I I I I I I I I I I I | HTTORC HTTORT |
| | 701 790 | | 810 | 820 | 930 | 840 | | | | | | | : |
| consend.report | CCONACANTECATTTACATTTTGGBA | TTOCATTTE | GBACTOGGTT | G016GARGGT | CAGTGGTANG | TECTTOTTE | TTGGTTGTR | CTGGGTTGGTGGTTGGTTGGTTGGTTGTTTGGTTGTTTGGTTGTTTGTTTCTCCATATCCGCTTGCTT | CCATATCCE | CTTGCTTAG | BSO TTTRIACTES | 900 | 910 |
| Rehfragnij821.12 primerpulation | CCGRACARIGCATTIGCATTITGGGA | TTGCATTITG | GGRCTGGGTT | GGTGGAAGGT | CROTGGTARG | TTCTTOTCTC | TTGGTTGGR | CT0000TTGGTGGARGGTACROTGGTARGTTCTTGTCTTTGGTTGGATTCATTTCTCRCCRTRICCRCTT- | CCATAICCA | | AATCTTTRICCGARTTTTTTOTTGCAGT | ARTTTT10T | TGCRGT |
| consens.clerectur | CCGNACINTUCATTTGCATTTTGGGN | CTTGCATTITG | GGACTGGGTT | GGTGGHNGGT | CAGT6GTARG | тосттатття | TTGGTTGTR | ETGGGGTTGGTGGANGGTACAGTGGTAAGTGCTTGTTTAGTTGTATAAATTTCTCGTCCATTTCCGCTTGCTT | ICCATTTCCO | CTTGCTTAG | TOTATABETOS | | -TTGCAGT |
| | | 930 | 940 | 950 | 980 | 970 | 980 | 056 | 1000 | 1010 | 1020 | 1030 | 9 |
| concent.repepdg | • | тваявтсттяс | CATTOTCTCT | яся втявас | ТСТСССТВВТ | TCAGAAGTAC | BIRCCTTCT | TOTCTCTRCRGTRIGGCTTCTCCGTGGTTGRGRAGTRCGGTRCCTTCTRCTTTRTTRGCCRICTCATRARGT-CTTGGGCRTR | CATCTCRIBA | ARGT-CT TG | BBCRTR | TCTT-16191 | 10101 |
| Rthfragmijj21.18 principGLint, principHijfI consenB.eletseedpGI | TTGCAGTGCGGTTGGAGTCTTACCTT TTGCAGTGCTGTTGGGGTCTTACCTT | TGGAGTCTTAC | CTTTBTCTCT | GCAGTATGGC: | ГТСТССЯТВВТ | Таявянатяс | затявсттет | TOTCICTOCAGIATOGCTICICCATOGTTGABAABTACGGTAGCTICIA-TTTATTACCCTICTCAGAGAATTICITAGGAABTAGGAAGTAATOCATGTGTGTCTGTC | стстсявна | АЯТТІСТТВ | GGAATAGGAA | атавтасята | TCTBTC |
| Cansonsus | | | | | | CHUNHUTHC | JOINCELLE. | | CATCTCATAR | nagt-crra | GGCRTA | 11011 | TCTOTT |
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Figure 16 BIS

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|---|--|----------------------------|---------------------------|--------------------------|--|--|-------------------|--|--------------------------|--------------------------|--|----------------------|---------------|
| | 1050 | 1080 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 | 1130 | 1140 | 1150 | 1160 | |
| | 1041 1050 | 2007 | | | | | | 111 | CTICICTITI | TTETTETETTTATTACATTEC | 1110 | GTTTTRTTTCRRARGTTGT | ROTTOT |
| | T1N1111CC1C1GRB1UM | TURBION | Toronotala | CTCGTTCTAR | CTATARRATG. | TCAGGABAGA | HATTGRIGIA | ARTICIBITI | TITITITI | TITICITIBL | ABITATELEGITETARETATARARIGICAGGARAGARATEGATATATETGIGITITITITITITITITITETTATETGATGATTCTTETTTTTTTTTTT | Tettettt | rerrer |
| AthfragaMJB21.12 pringrPGI.intl | | | | | | | | 111 | CTTCTTTTT | TTCTTCTTTTTTATOCATTCCC | CGTTT | GTTTTATTT-CAAAAGTTG1 | явотта |
| | TTATTTTCCTCTTBATGR | | | | | | | | | | | | |
| | : | | 0007 | 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1200 | 1290 | 1300 |
| | COCTGTCTCTARATCARGARACCTT | CREGREGAR | CCTTCT-TR | атнаятсся | TORTRITCAG | CT-TRGTRGRICCAGIORINITCAGCCTTTTCTART | A1 | GGRCTGCAGG | TTTTTABAGE | О ВВСТТСЯВО | TOGRETOCROOTTITTARROODROCTICAROCRITGRICAGERITTECNOTEC-ERE | CRITICEN | זככ-כת |
| Principal Intu | RCTTCCCTTTTATTTATTRCCCTTCCCT | TATTRECETT | CCCTATOTTI | СТАВЯТССЯС | явтявтосяв | тсаятяттся | GICTITITI | 60A100TAG(| ITTTTGARGO | GRECTTCARE | ATOTTTCTARATCCACARTAGTGCAGTCGATATTCAGTCTTTTTTTGGATGGTTTTTGAAGGGAGCTTCAAGGCATTGATCAGLATTTCCAGTCCATTG | SCRITTICCER | TCCRCR |
| primerPGILDIL | ссвасссстинассяванинестт | CCRAGINGINI | ICCTTTC-TAGGM- | IGGNCCRGR | i | стесяссеттттяяят | | GBACTGCAB | ITTTTABBG | GGGCTTCANG | TOBACTOCROOTTTTAARGGGGCTTCARGCATTGRTARGCATTTCCROTCCACRC | CONTINCER | TCCACA |
| | | | | | | | | | | | | 5677 | |
| | 0161 1061 | 1320 | 1330 | 1340 | 1350 | 1360 | 1370 | _ ! | 1390 1400 | 1400 | 74Y | | TRGTGT |
| ConsenB. reperci | C-GTTTGRGARGARTRIACCCCTGRGTT | ATRINCCC010 | RETTECHTT | HETTOTOTION | GCATTAGTTG1GTGATTATACAG1-TTTCTTG | TTCTTG | TCTTTTGC7816- | 1 | ALTECAR. | THE TREETT | GCATTAGTTGTGTGATTATRCRG1-TTTCTTG | TRECARGER | TTRCA |
| PrimerPGIIntu PLHFragnHJ821.12 PrimerPGIInt PrimerantiPGIL | C-011CGAGAGANTATACCTGTGAGT- CCG17TGAGAAGAATATACCCGTGAGTT | NTRIRCCTOTO RIRIRCCCOTO | 3AGT-GCTTTI BRGTTGCATT | ATTTTGATAR AGTTGTGTGA | actttattttantarcactaaangtactg GCATTAGTTGTGAATTATACAGT—TTTCTTG | | .CRTCATTTMCANNUM. | 1CAMBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB | -TGAT CAACCTAGAGATT -CGT | ABBRTT-CGT | | | TAGTG |
| Consensus | | | 027 | 1470 | 1480 | 1480 | 1500 | 1510 | 1520 | 1530 | 1540 | 1550 | 1580 |
| | 1437 | | 4] | | | | | | | | ſ | . ! | |
| prinerPGIIntU | | GATTICTOTA | Ē | ATTRGTGTRG | тсясассевя | AGTTTRATTRGTGTAGTCACCCGGAGTGABAGGTTGATTTGGTGACTTTTGACGATTT | аяттаатан | CTTTTGACGA | | TTTTAGGGTT TTTTAGGGTT | CAGGTGCTTTTAGGGTTGTTGTBTATGGAATGTATGTTGTTTCTTTCTTTCTTTCTTTCTTTC | тванятатн | |
| principalinal principalinal principalinal principalinal | | REGREC | • , | | | . • | • | | pPGlintl | nt! |] | | |
| prinerPGIU | | | 06.1 | 1800 | 1810 | 1620 | 1630 | 1840 | 1650 | 1660 | 1670 | 1680 | 1690 |
| Ting a control of | | | | | | | | | . (| | .oogercatet | racettati | THE PROPERTY. |
| SCHOOL STATE OF THE SCHOOL OF | TGGNTNTCCTGCTAGGGIANGRATCGR | T AGOOT AAGAA | | гтатсябяяяс | ЗСТВВВВТТТ Т | гсатстсявт1 | твясятятіс | AGCCTCCAT | CAACATCTTT | | CTCCTTTRICAGRARGCTGRAGTTTTCATCTCRGTTTTRAGRITATCRGCCTCCATCARCATCTTTTGTTTTCTCTCTTTGTTTTCTCTCTCTTTTGTTTTCTCTCTCTC | | |
| Consonsus | | | | 1730 | 1740 | 1750 | 1760 | 1770 | 1780 | 1790 | 1800 | 1810 | 1820 |
| consent.repetation | 1691 1700 1710 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | CTCCACACAT | | TOTGRACTEG | BTTTCCCTTT | TBTCTCCTTR | ATC1T1GCT1 | TTCATATCT | ATTTTORCA | тававатстт | CAGGTATGTGARCTGGGGTTTCCCTTTTGTCTTTGCTTCTTCATATCTTTTTGACATARAGICTTAAAATTTTACGGGAATATTAACGGAA | Асваваятя | TTRACE |
| ACHITAGANICELTUT Primarantifoli Primarantifoli Consend. Olaracoppi | | | | | | | • | | | | | | |
| Consensus | | 1840 | 1850 | 1860 | 1870 | 1880 | 1880 | 1900 | 1910 | 1920 | 1830 | 1940 | 1950 |
| Consend reporti | CANTIONICYCROGITRGIBIOGRARGGRANGGGRATCICARTIOATGGTCTRCCTCCCGTTCGROACTGGTTGATTTTGGTGARCCTGGRACARTGGTCARCACACTTTTA | TEYCAGGT190 | ITATGGABAGI | IARTGGRAAGG | IGRGTCTCART | товтватств | וככזכדכככמז | TCGAGACTG | товсяттся | TTTGGTGAAC | ставяясяя | TOGICARCA | CRACT |
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Consensus

HipsAt162850ant.1 SeqAc007190fin-AC011 GCPATPB01JU

Consensus

ANGGSPARAGTRITAGARCHICTARARACTACARTGARABTARGSTARAGGCACARGARCARGGTCACACATTTGTTCACATTCTGGCCTCCAGGACCACCTCTTCTAGCARAGGTTARGTT

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> HipsAt162850ant1 SeqRc007130Fin-AC011 GCPRIpBolJU

Consensus

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overlapping

| 1040 | | |
|---------|--|--|
| 1030 | ATREAGRACTIC BTREAGRETTC BTREAGRETTC BTREAGRETTC | |
| 1020 | MACTCAGTIC MACTCAGTIC HACTCAGTIC | |
| 1010 | HEXIGNTININCRETENTINACCONTTTENTITENGITCATGININCOGATENTCATTGGCTCTACTTONACTCATTCATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGA | |
| 7000 | GNTGNTCATT GNTGNTCATT GNTGNTCATT GNTGNTCACT | |
| 250 | CATGTATACA Catgtataca Catgtataca Catgtataca | |
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Consensus

| | | Bollon U about 700bp | fromAC00719 end |
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| 1 10 20 | | 261 270 280 230 300 310 320 330 340 340 350 300 300 300 300 300 300 300 300 30 | |
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Figure 17 BIS

| | Bollon | antil. | from AC011000 | start | | | | | | | |
|-----------|---|-----------|--|-------|---|-----------|---|--------|---|-----------|--|
| 1170 | | 1300 | RETGR | 1430 | 1600 | 1560 | | 1630 | GGTGAT | | : |
| 1160 | TCATT GCCAGCGGAACT | 1290 | ATCTGTTGCACCTGCACARCCGTGARGAGACTTTCCGATCACCACCGCTTCCACCGGAGGTCGATGCCGCACATCGGACGGA | 1420 | GGAGACRIGGIANARGAGATTEACACGATTTCGATGAAGTGAAGTGAAGTGGATGATGATGATGGATG | 1550 | TEANGATIC TICCEATETCARRATGACGATGTCAGAGGAGGAGGAGGCGACCCTAATTTTGCGTGGCTCCCAATTTCCGGTTTACGGTTAGTAAAAAA | 1680 | .TTTARARCOBTCOGGTCARARTCARARCOCGATTTCCGGTTCATARTTCCGGTTCGCRTCACCARCAGGATTARGTTRGATTRACTARCCTARC | | |
| 1160 | | 1280 | GGRTRCGR | 1410 | CATGTTCG1 | 1540 | TTCCGGTT | 1670 | TTRGARCT | | |
| 1140 | NGACTGATTTGAGGAGTAGG T-AGGGATTTTGGGGGT-GG | 1270 | CCGCACATCGGAC | 1400 | CTCGCGTAGANT | 1530 | ICGTGGCTCCCAR | 1660 | CARCGCARTTARG | | |
| 1130 | MGCTTGCCT MGCT-GCCT Seget.gcc | 1260 | RGGTCGATGO | 1390 | ATGGATGAB | 1520 | CTRBTTTE | 1650 | GETTCGCBTC | | |
| 1120 | ARRAHARIN Renirahari Babbababa | 1250 | TTCCRCCGG | 1380 | ARGTGGATG | 1510 | вянсесенсс | 1640 | ATABITTCC | | |
| 1110 | ATGARAGCA ATGARAGCA atgassca | 1240 | וכאככאככנכ | 1370 | AGTGANGGAC | 1500 | GARGARGAR | 1630 | TTCCGGTTCATAB | • | |
| 1100 | TTTCARRIGG TTTCARRIGG ttcaaatga | 1230 | ACTTICCGAI | 1360 | TCGRTGRAG | 1430 | тотсяения | 1620 | REINCOCORT | | |
| 1090 | LIBITCCTTRARRCTRANCTCRGTTCTTTTTTCRRNGGRTGRANGCARARARARARAGCTTGCO LIBITCCTTRARRCTRARCTCNGTTCTTTTTTTGARTGGRTGRANGCARARARARARARAGCT-GCC ctallcctlabasclabacloaglilctlilttcasalggalgbasgcabasasasasasagci.gcc | 1220 | CCCTGARGRG | 1350 | TGACACGAT | 1480 | TEANLATTC TTC CGATGT CARRATGACGATGT CAGAGAAGAAGAAGAAGAAGAGGCGA | 1610 | GTCRARATTC | <u>بر</u> | - = : |
| 1080 | HRECTRINET HARCTRARECT Basctraact | 1210 | CCTGCGACAA | 1340 | 7811AFACAGA 1 | 1470 | TCC68161C | 1600 | ятссватся | 1730 1735 | GACARCTCTCAGARATCTATA |
| 1070 | TRITCCTIR | 1200 | ATCTGTTGCA | 1330 | GGAGACRIGG | 1460 | TGARGATIC | 1590 | CTTTRABACG | 1720 | GACARCTCTC |
| 9960 | -CRI TCCRTRRC TCCRTRRC TCCRTRRC | -4- 65 | NGCTCTCTCGGCTTCA1GANGC | 1320 | ATT GGAGARATT AGGGGAGT GAGAC | 1450 | CCAITITETTIATCTTTCTCGGCAC | 1580 | CGIRACATTTCTTGGTTTRICT | . 01/11 | CRTAGCARGTACAGAGTATCTCGG |
| | II CRHARBEI HGRBT II Dicabbibli Bgartti Micabairgingenitte Atcararbistatite | | CTTCGGCT | 1310 | IRRITTRGG6 | 140 | TTANCT | 1570 | ATTTCTT | 1700 | MGTRCAGA |
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